

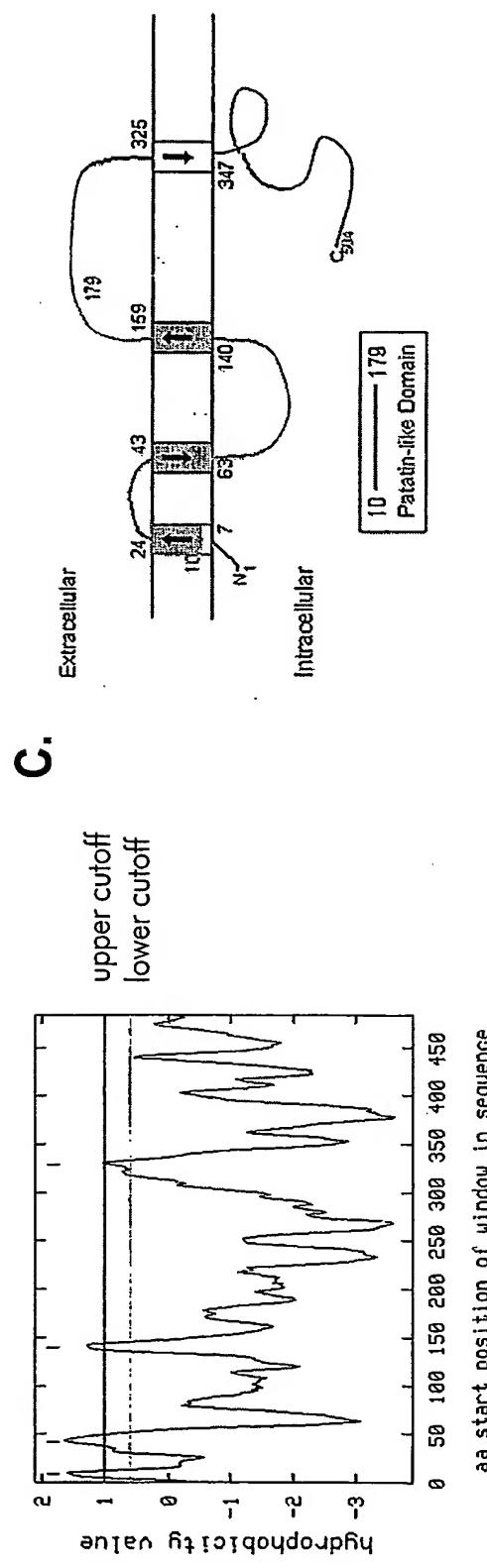
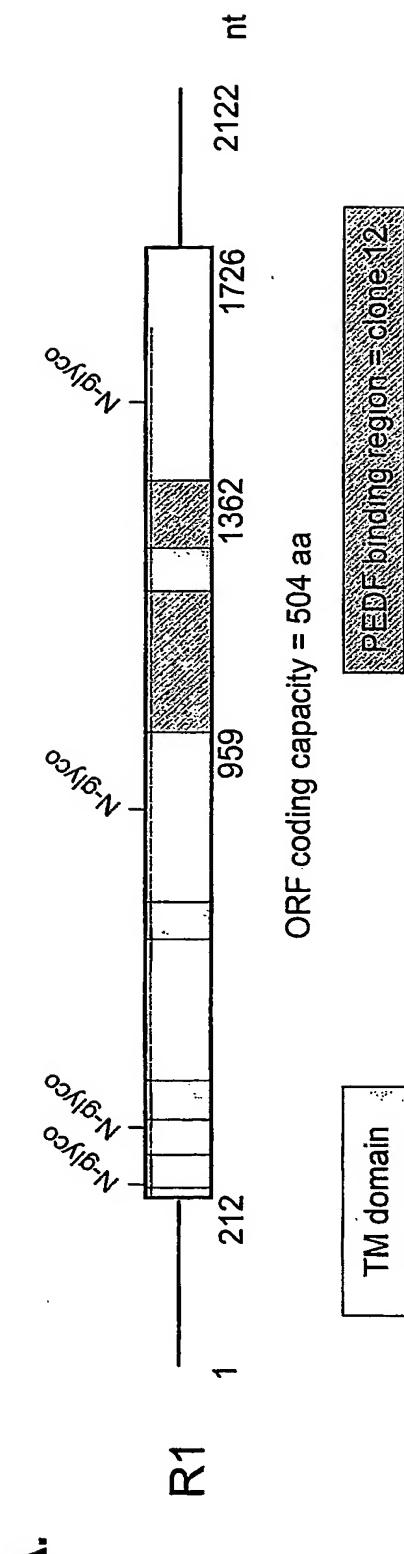
Figure 1.

Figure 1.**D.**

R1 MFPREKTIWNISFAAGCGFLGVYYGVASCLREHAPFLVANATHIXYASAGALTATALVIGVCLGEAGAKFTEVSKEARKRFLG
 adiponutrin YDA RG SL F H ATR H LRD RMLF HCVGVL S I P EQTLQVLSDLVRK S NI
~~PLHPSENLVKITRSFLKVLPADSHEHASGRRLGISLTRVSDGENVILISHENSKDELIQANVCSGFIPVYCGLIPPSLQGVRYV~~
 IF S FL QG C C NV QLI KI LV DFR VVD

L	C	F	S	FR
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DGGISDNLPYXELKNTITVSPFSGESDICPQDSSTNIHELRVTNTSIQFNLRNLYRLSKA LFPPEPLVLREMCKQGYRDGLR
 V V FIDA T P Y Y KV KVK FLHVDI KL LRLCTG L R FV DLK G I LR L AF

FLQRNGLLNRNP-LIALPP-----ARPHGPEDKDOAVESAQAE--DYSQLP--GEDH-ILEHLPARLINEALLE
 EEK IC Q G KSSSEGMDPEVAMPSWANMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLTTLSNMILPVURLATAMVPTYLPLESALSFTIRLLELPDVPEDIRWMKEQT GSICQ YLVMRAKRLGRELPS
 EMRKDKGGMMSKIC I

I	IMSYV	L	C	V	IAIVQ	VT
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 MD VL IQWV SQVFTRL CLPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAAYREALPGWMRNNNLSLGDALAKWEECORQLLGLFCTINVAFFPEALMRAPADPAPAPAD
 SSQQASPCTPE DW CWT C PKGCPAETKAATPRS I RSS NFLGNKVPAGAEGLS --- SFS EKSL-----

PASPOHQLAGRAPLSTPAPEARPVIGALI

E.

253 GLINRPN PLLALPPARP HGEPDKDQAV ESAQAEDYSQ LPGE 293
 450 T NVAEPPEALR MRAPADPAPA PADPASPOHQ LAGPAPLIST PAEAPPVIG ALGL 504

Figure 1.
F.

Homologous patatin phospholipase A (PLA) active site in R1: S47 and D166

Active site serine

NA	THIYGASAGA	LTA	R1
YF	DVIGGT S TGG	LLT	Patatin B2
CA	TYVAGL S GST	WYM	cPLA2

Active site aspartic

SIQ	GVRYY D GGIS	DNLPLYE	R1
ARY	EFNLV D GAVA	TVGDPAL	Patatin B2
KSX	KIHVV D SGL-	TENLPYP	cPLA2

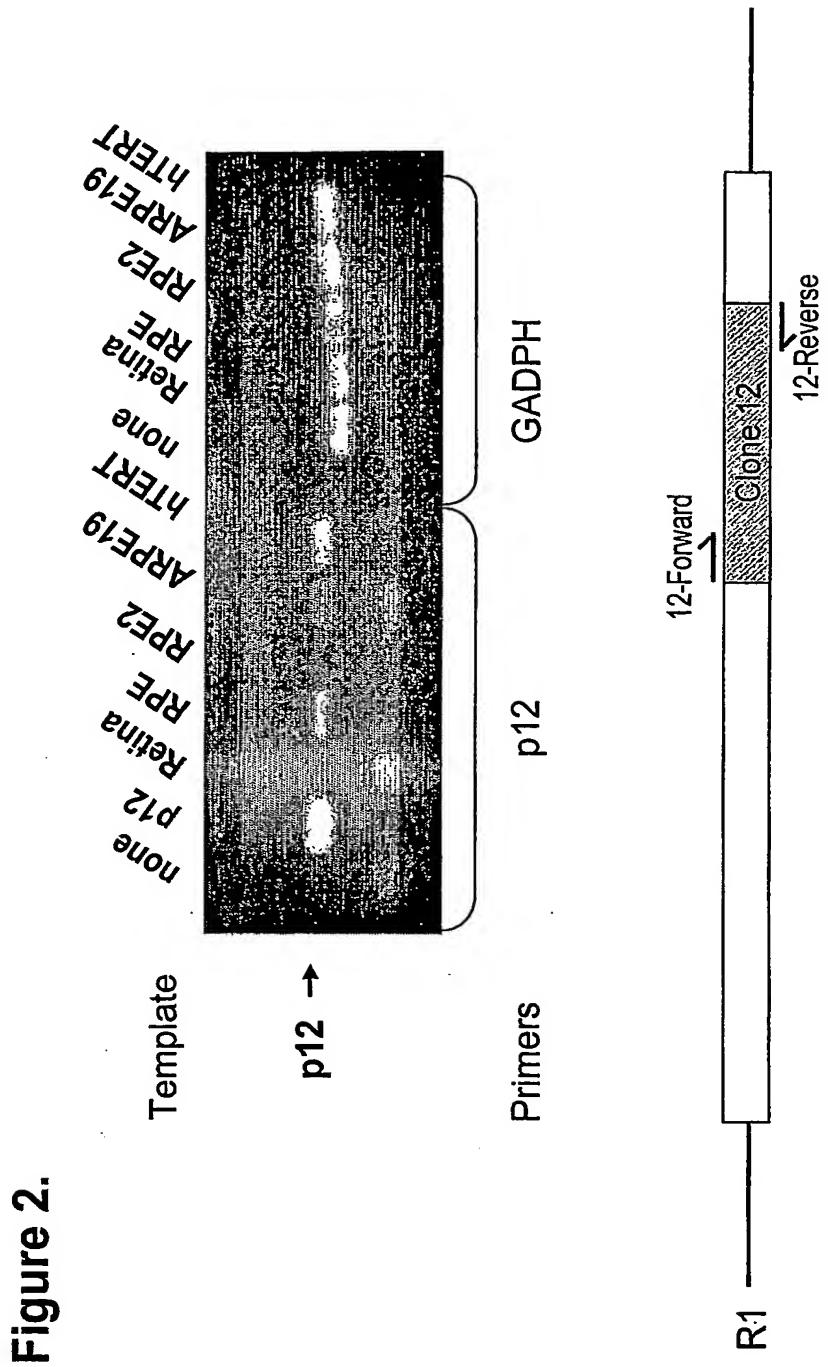


Figure 3.

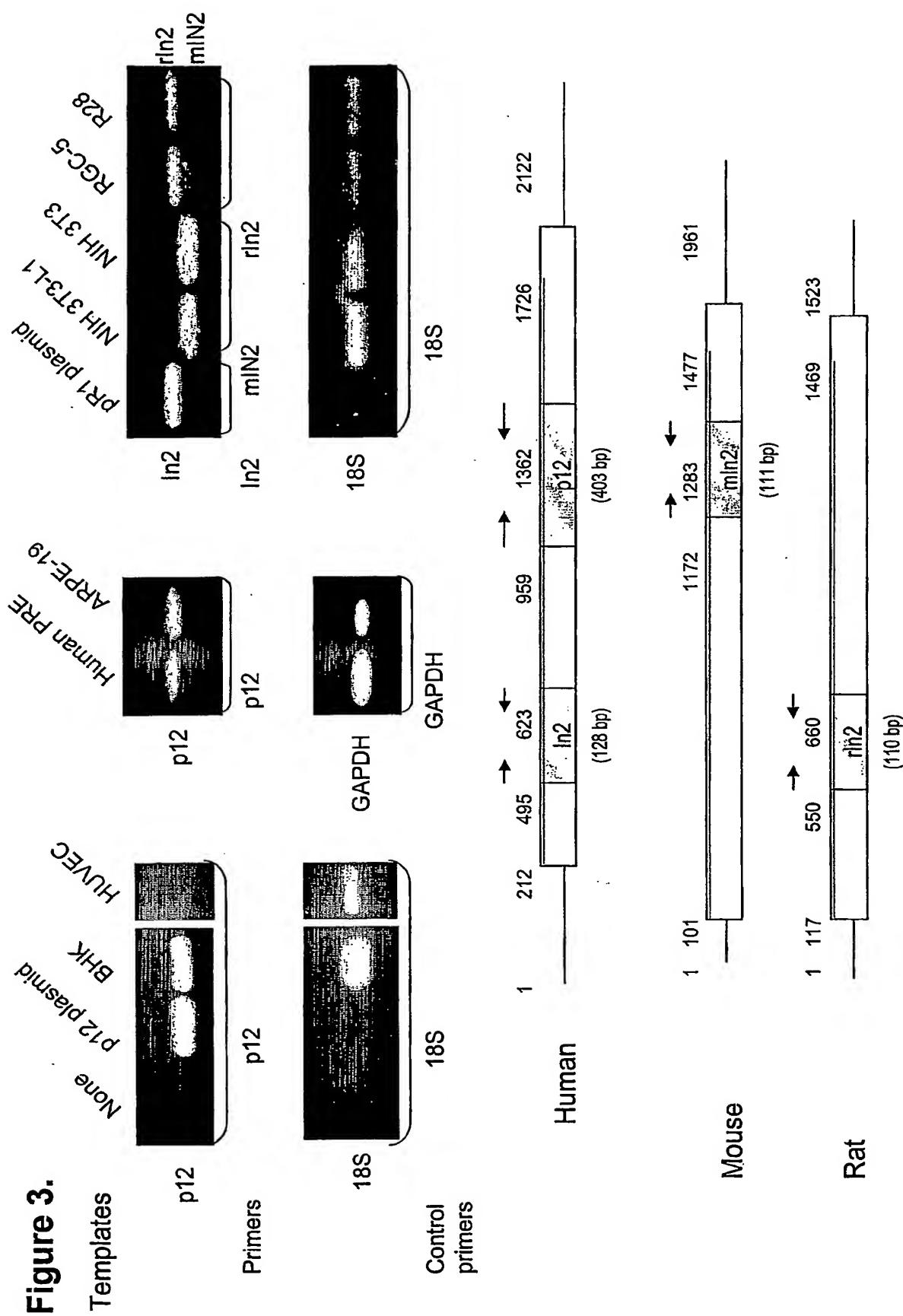
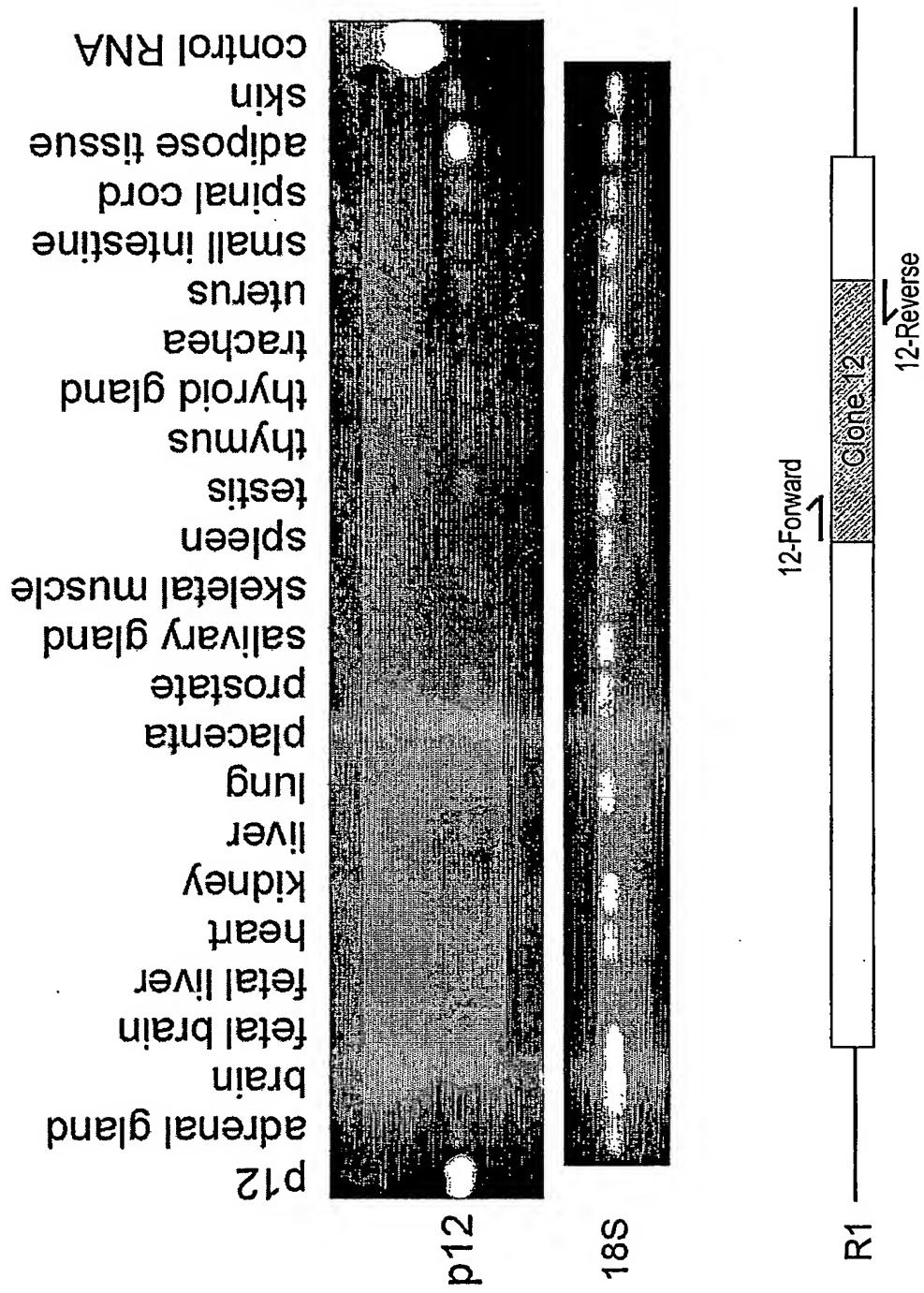


Figure 4.

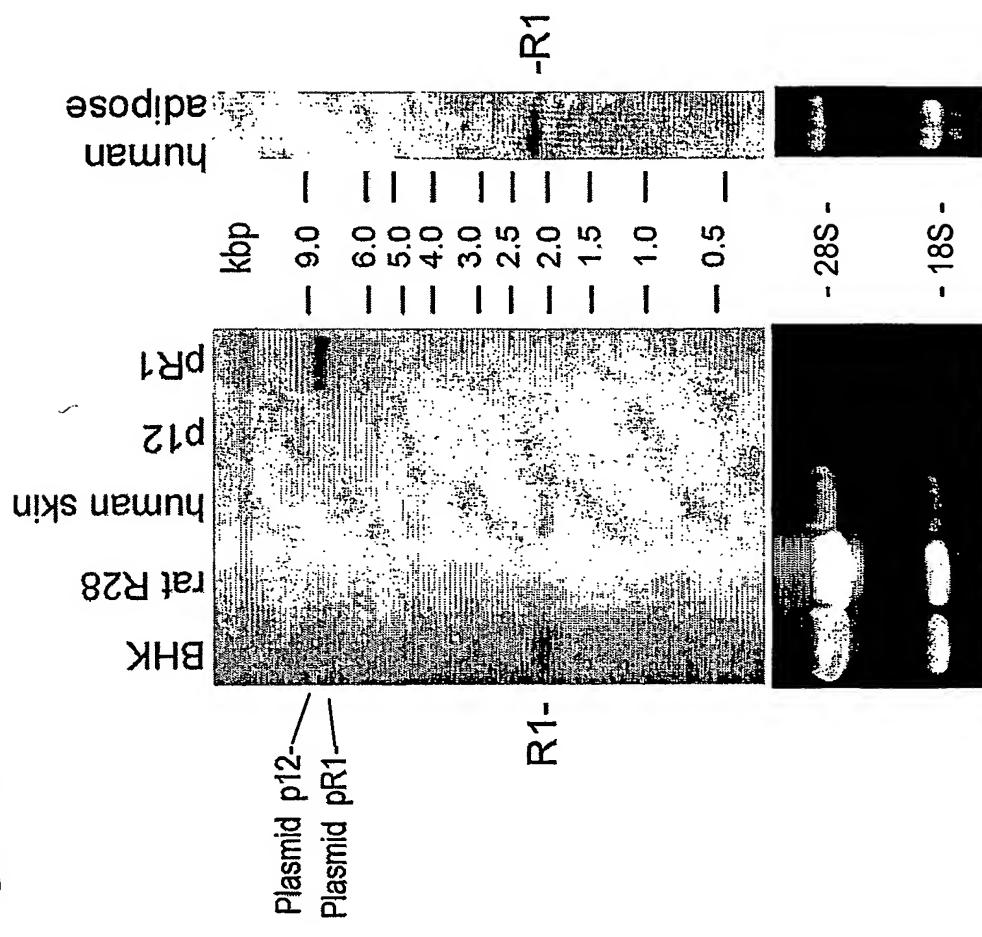


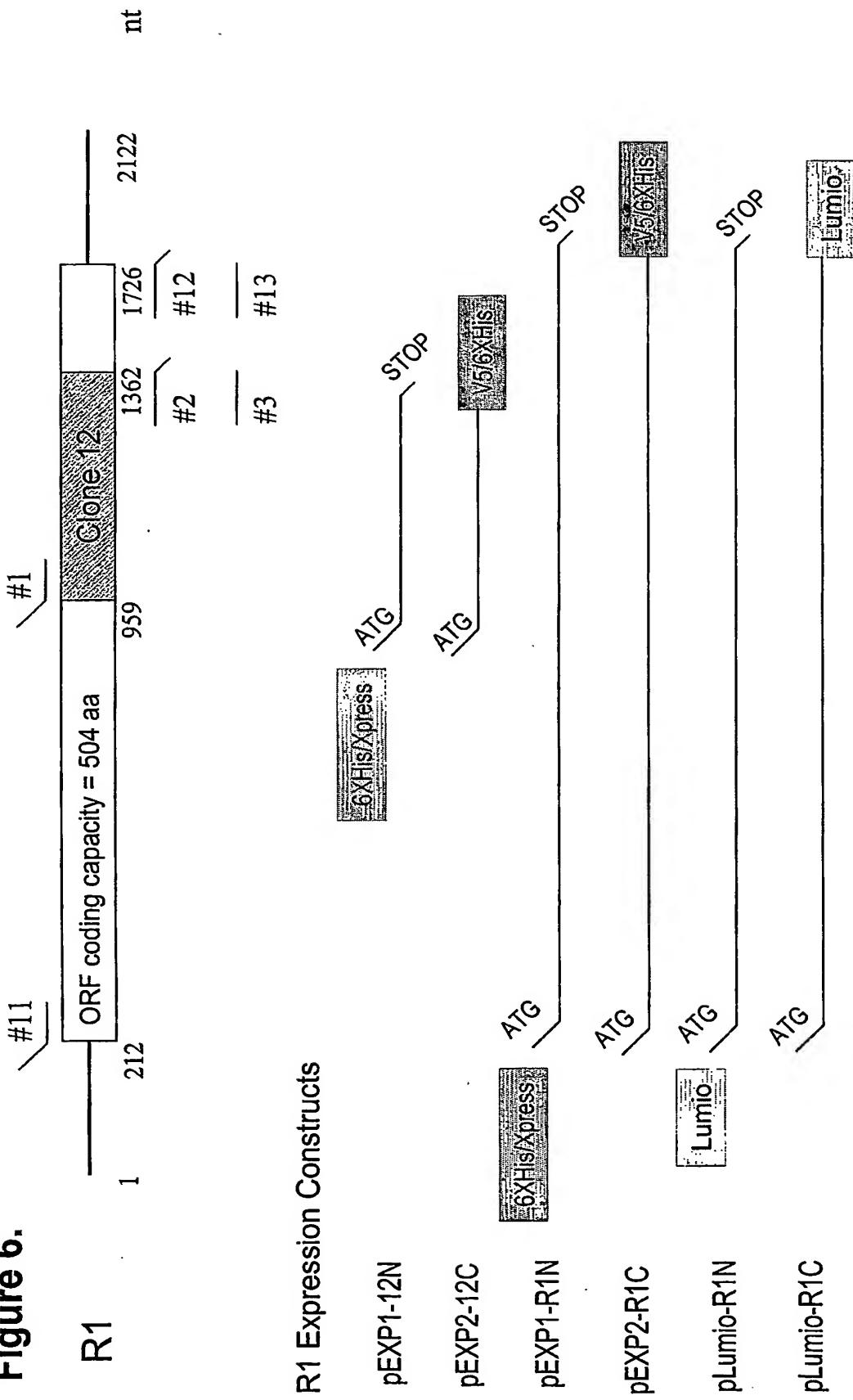
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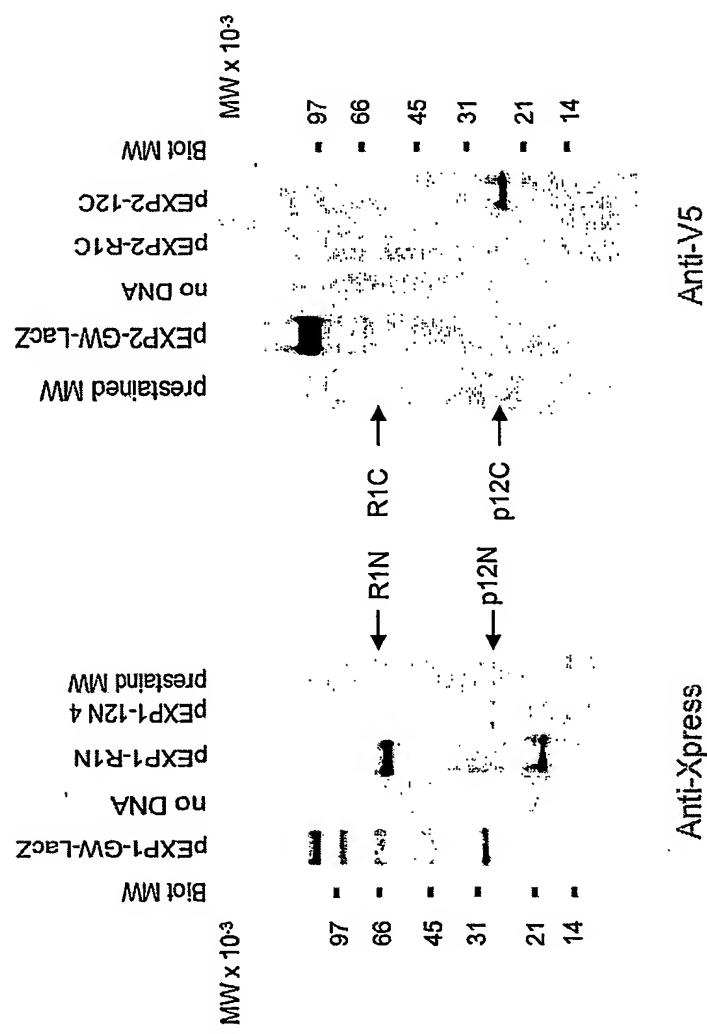
Figure 7.

Figure 8.

A. p12
Chromatogram

**SDS-PAGE
 (Magic Blue stained gel)**

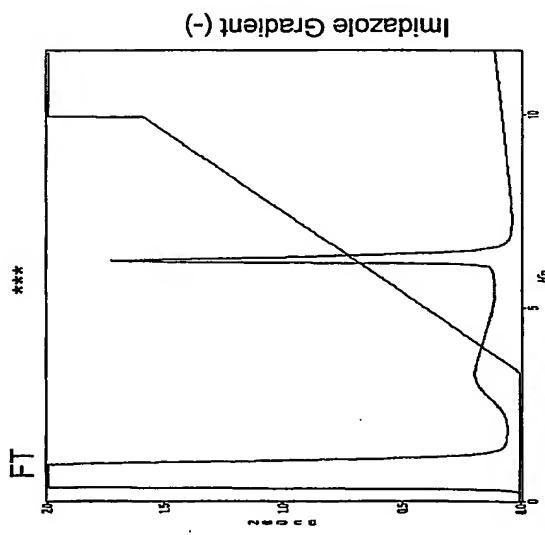
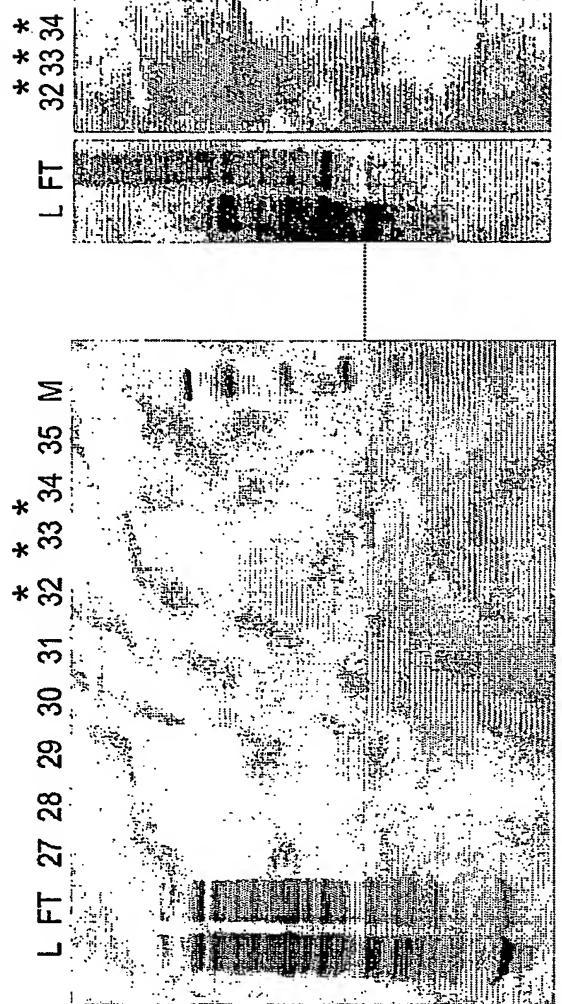


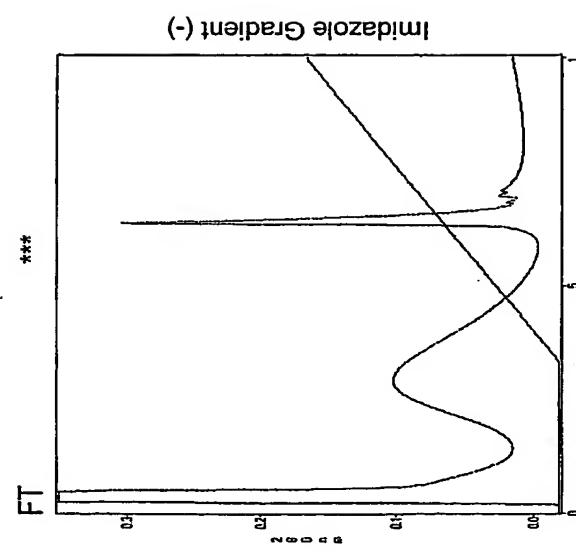
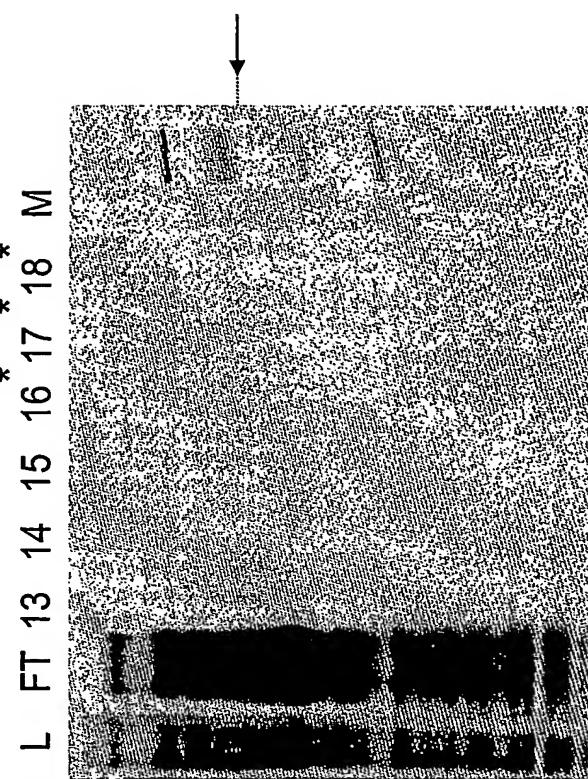
Figure 8.**B. R1****Chromatogram****SDS-PAGE (Coomassie Blue stained gel)**

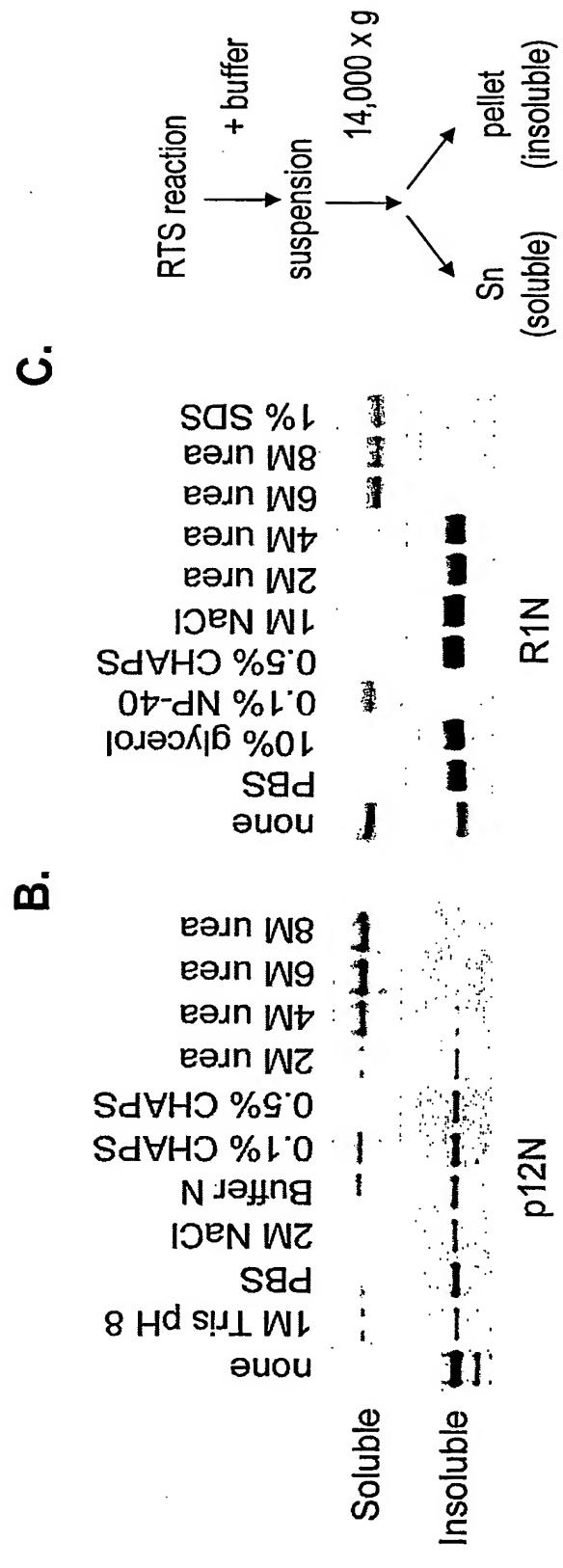
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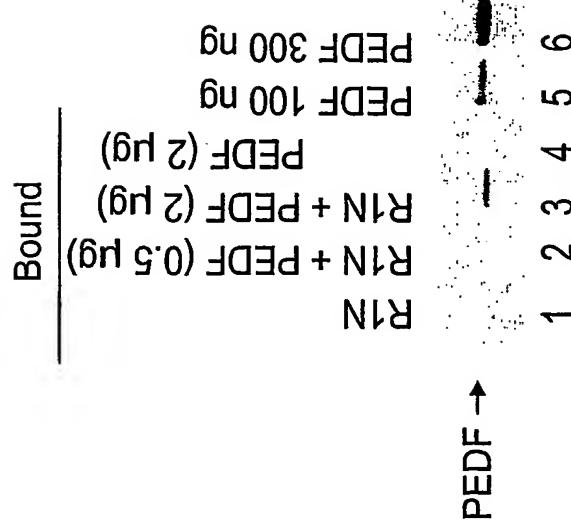
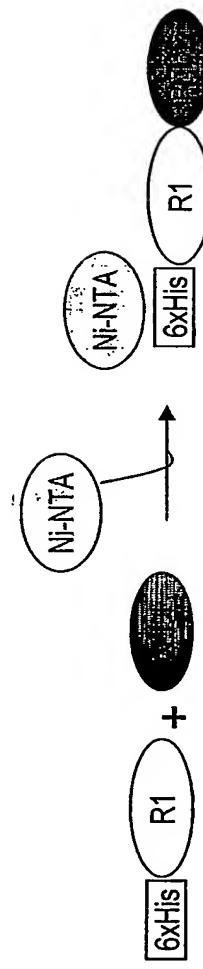
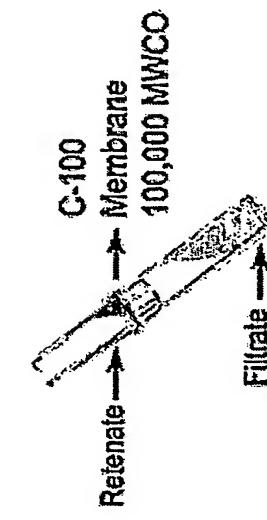
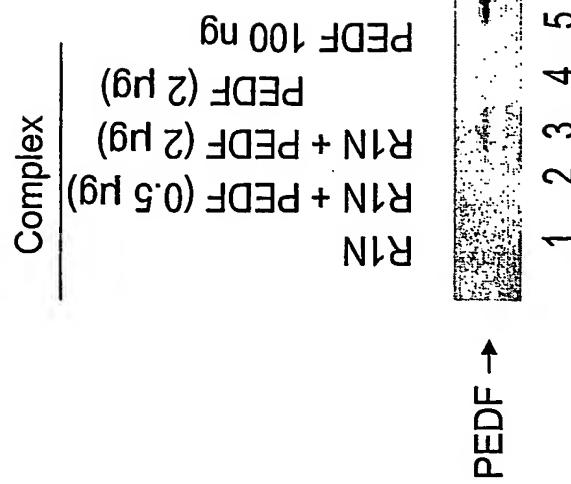
Figure 10.**A. His-tag pull-down****B. complex formation**

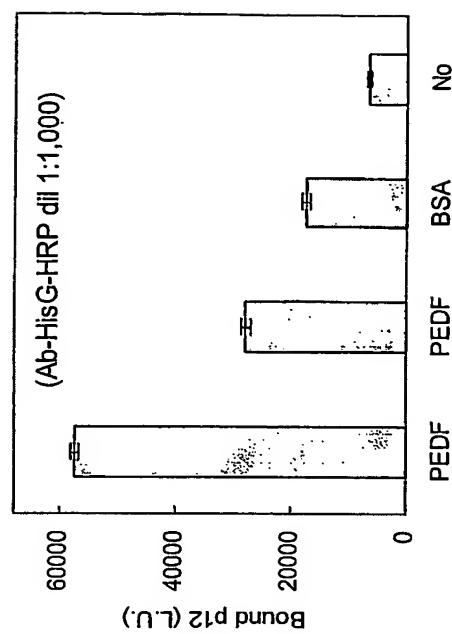
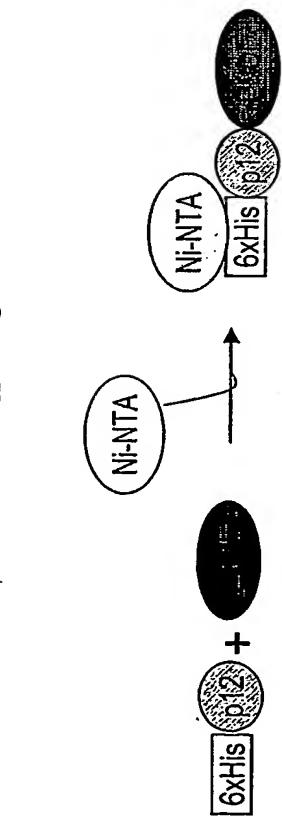
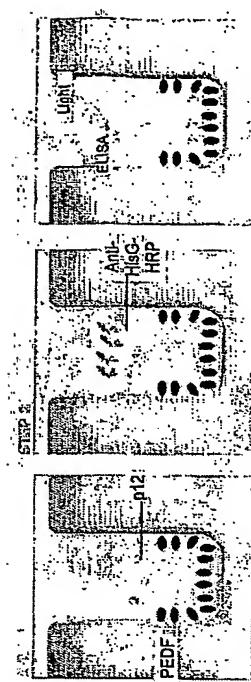
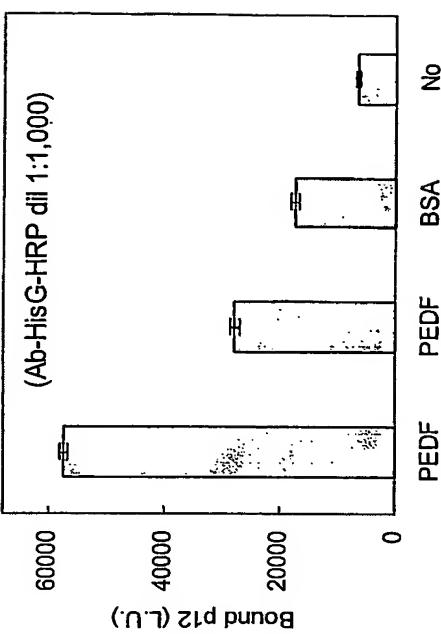
Figure 11.**A.****B.**

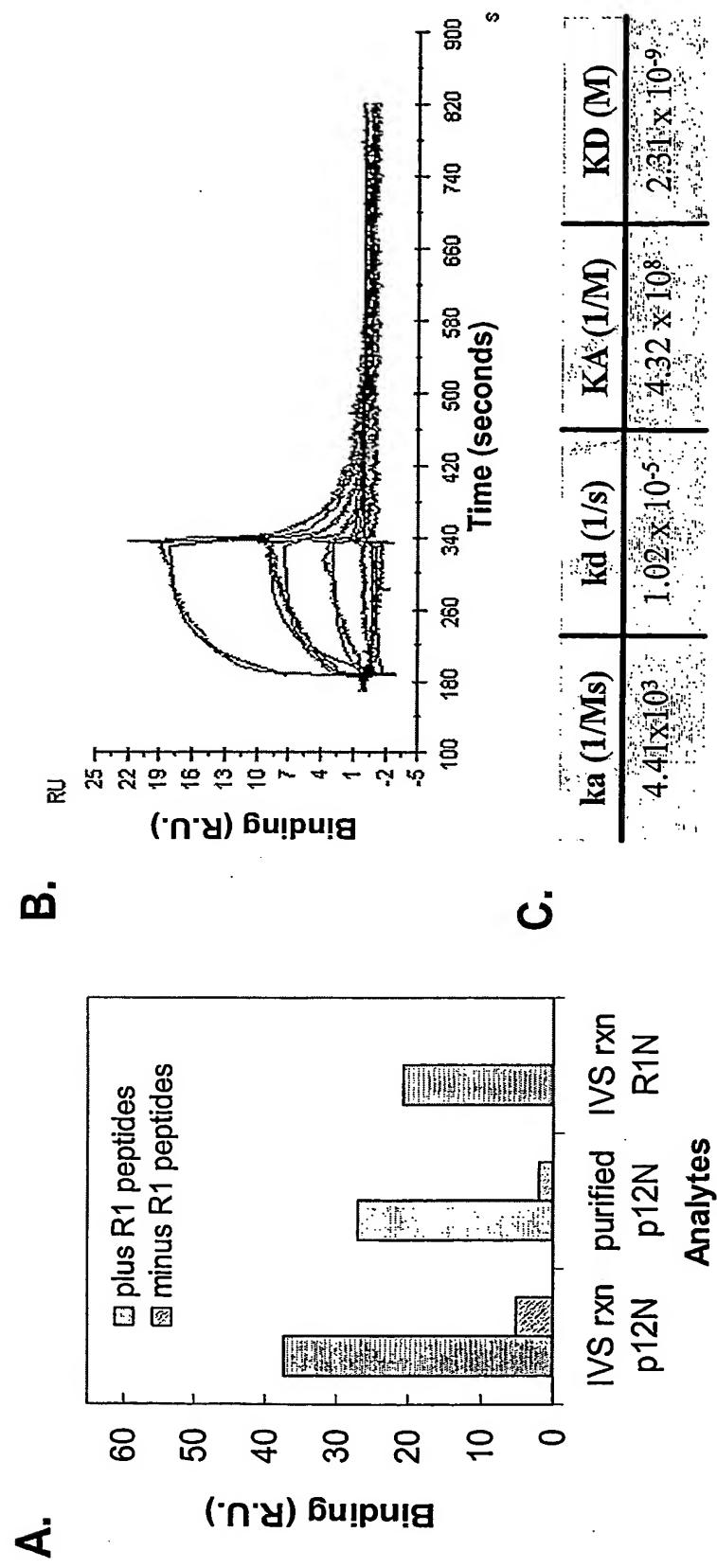
Figure 12.

Figure 13.
A.

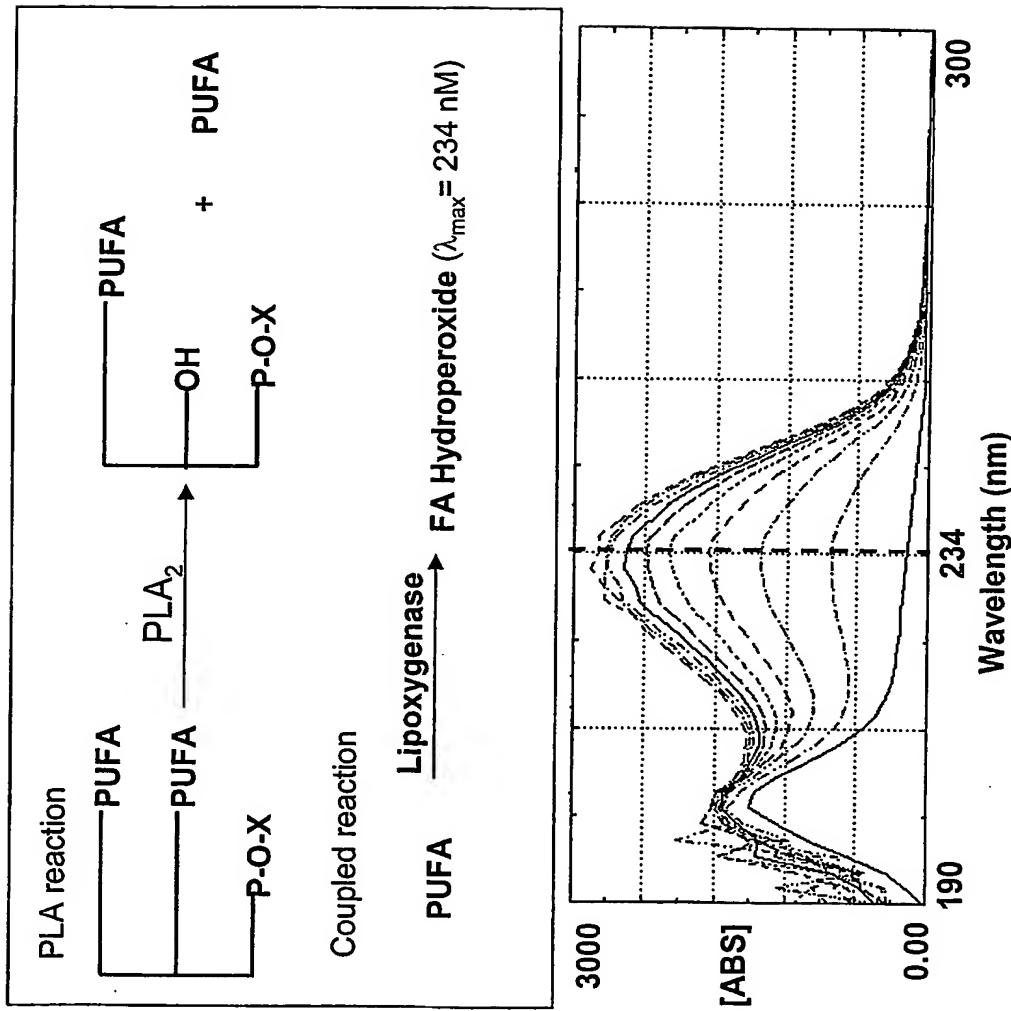
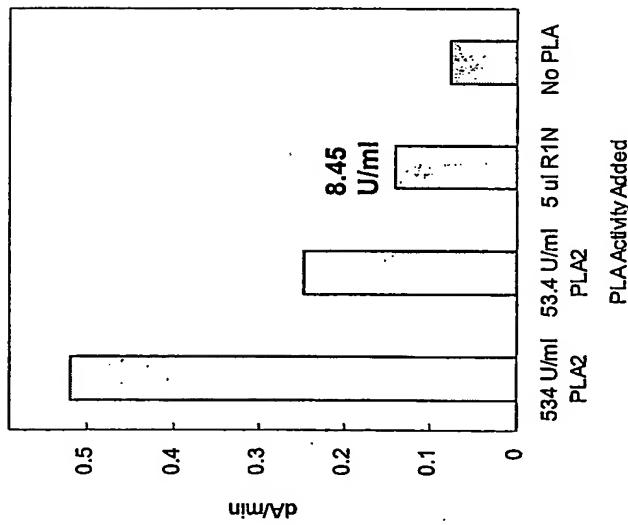
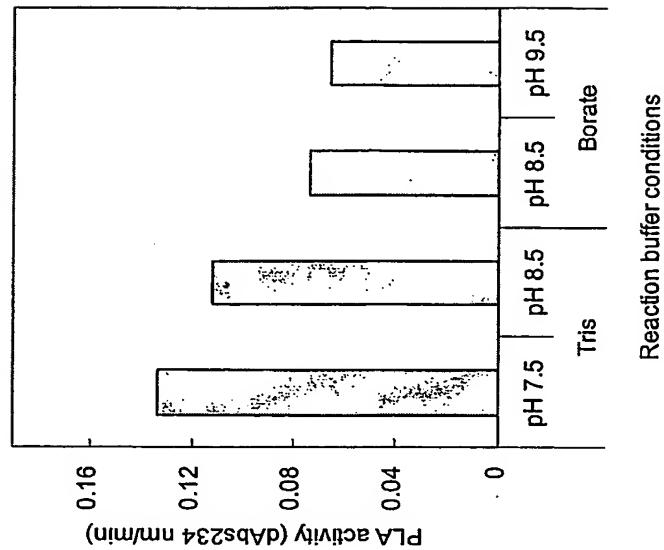


Figure 13.**B.****C.**

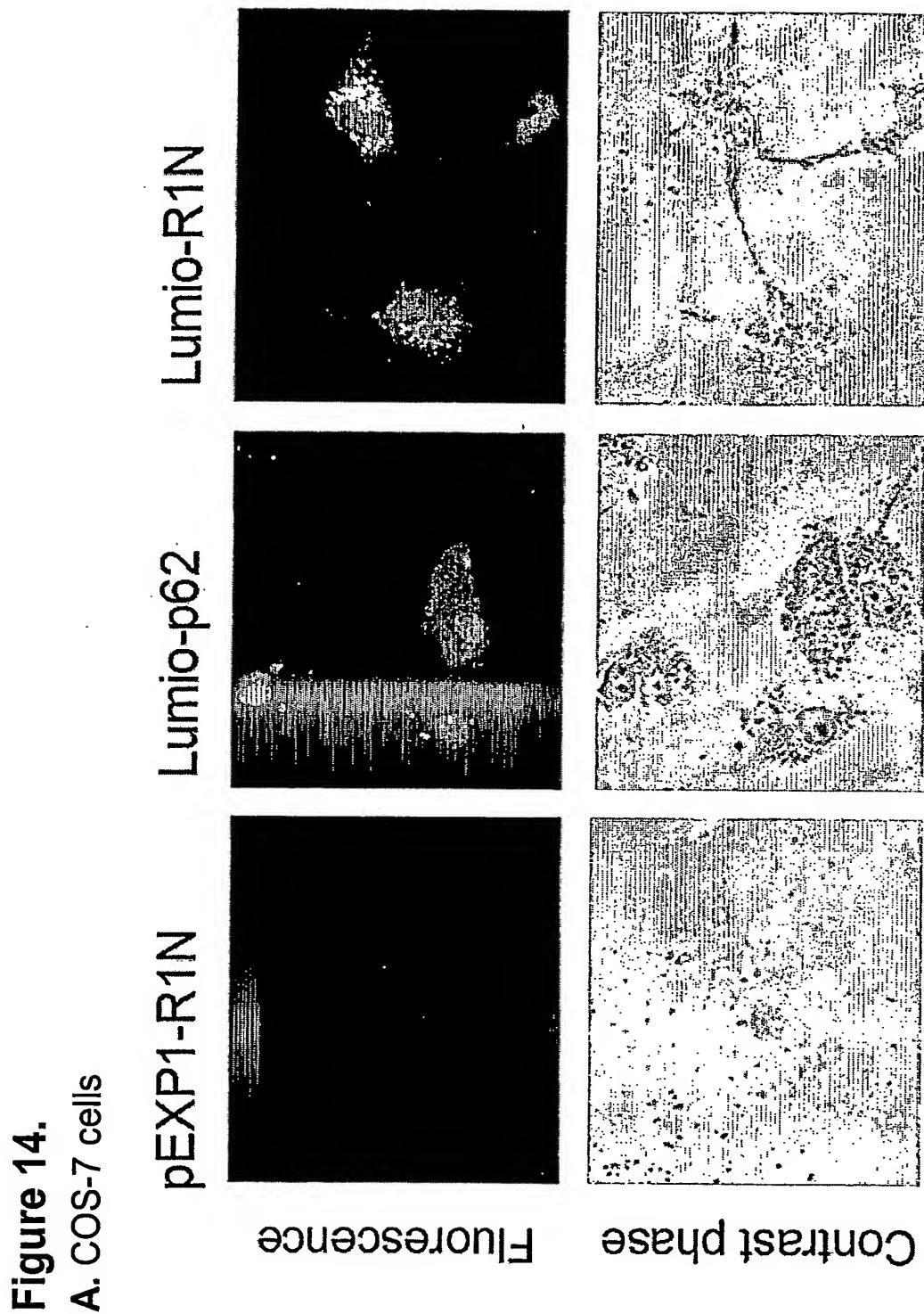


Figure 14.
B. Retinal ganglion RGC-5 cells

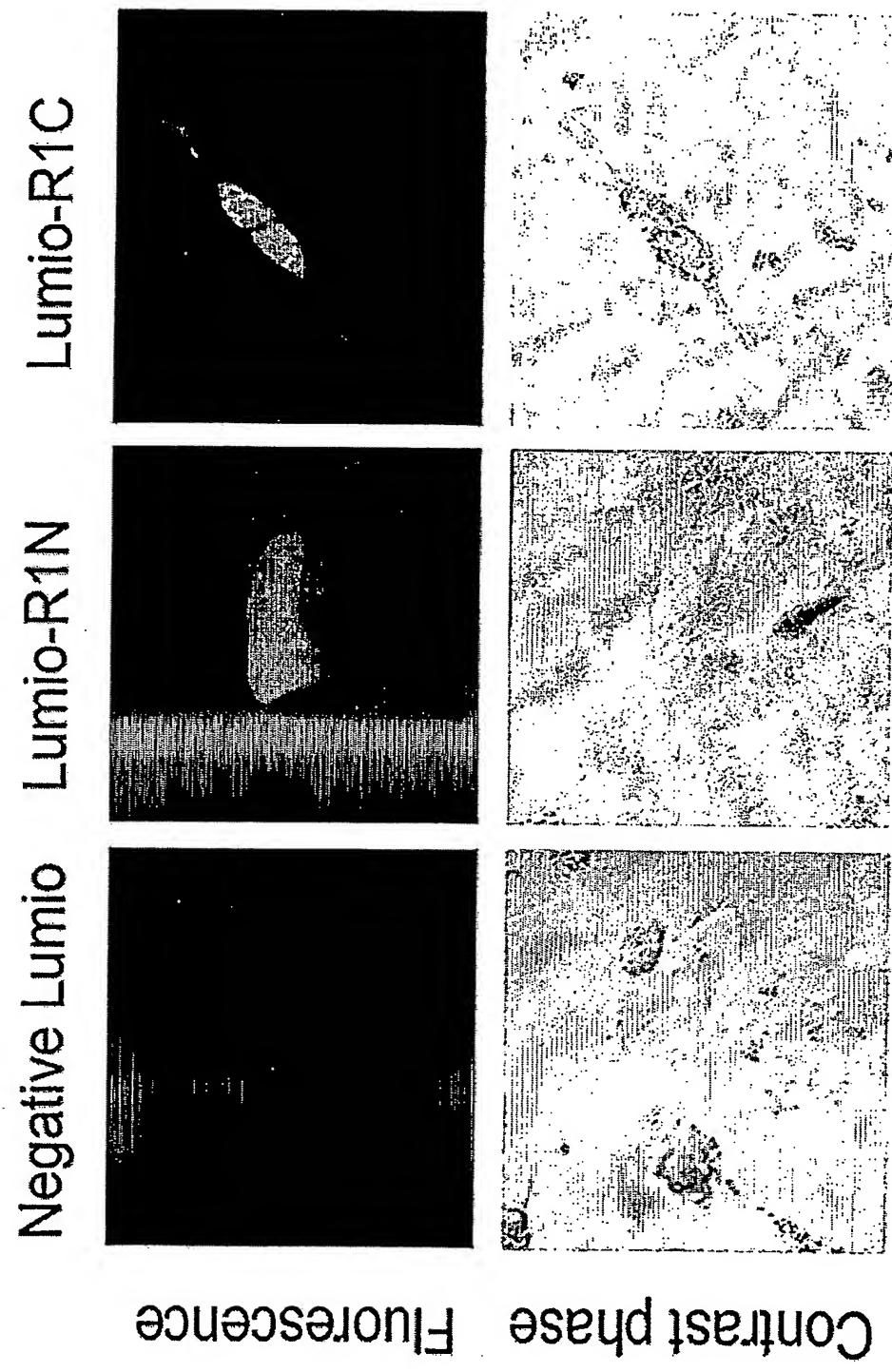
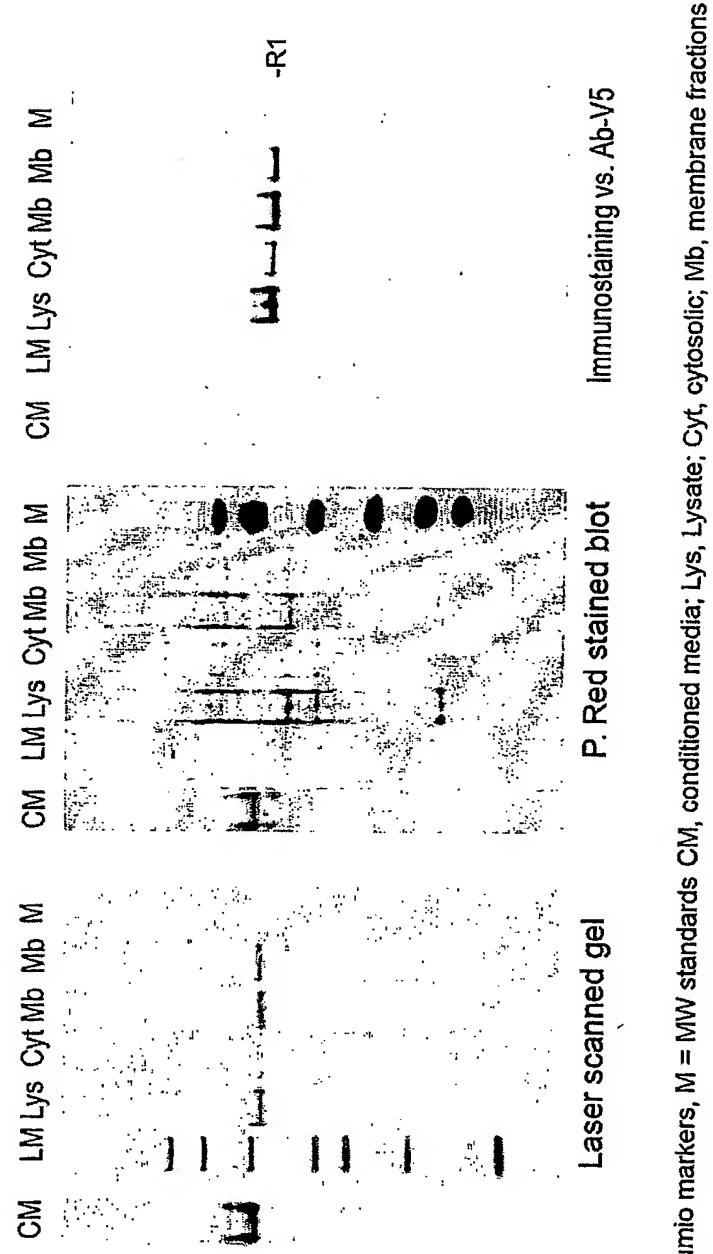


Figure 15.

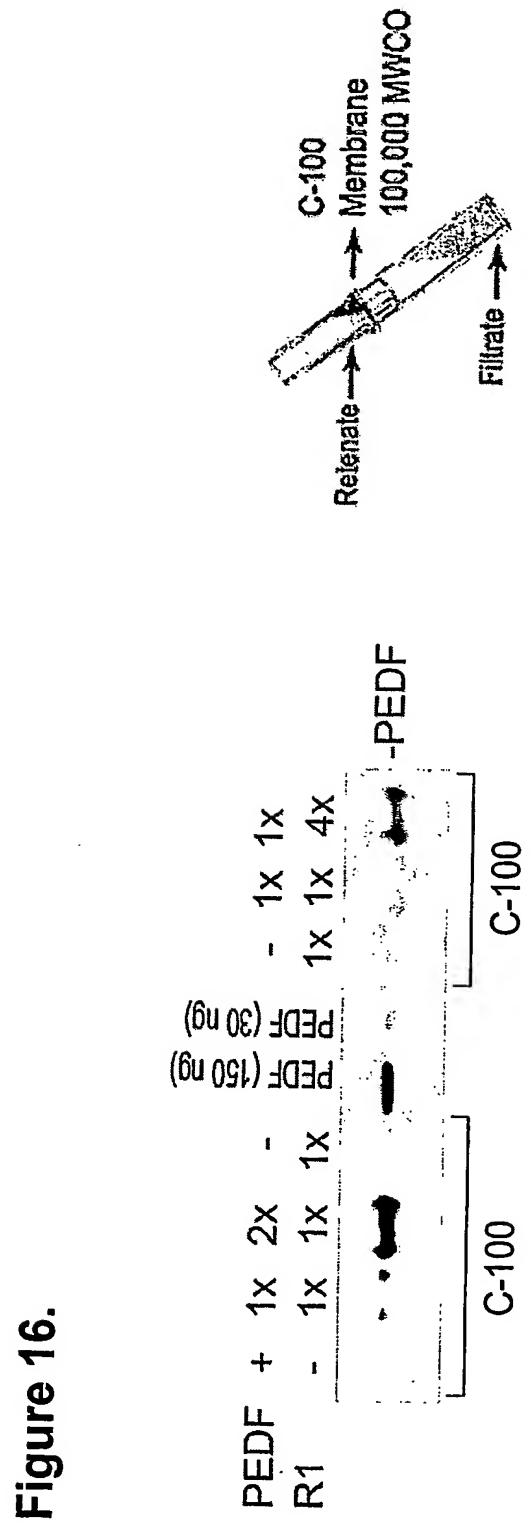


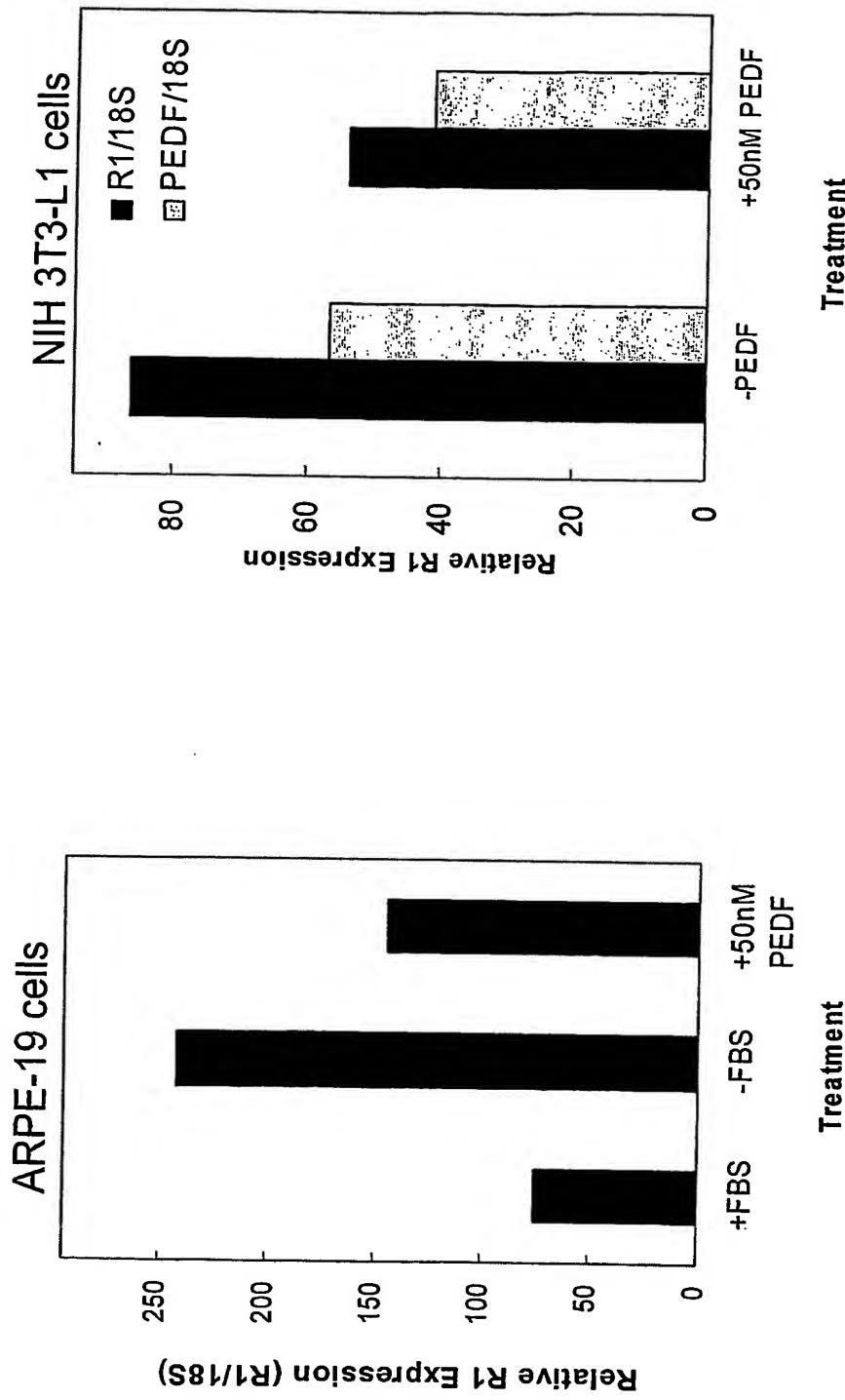
Figure 17.**A.**

Figure 17.

B.

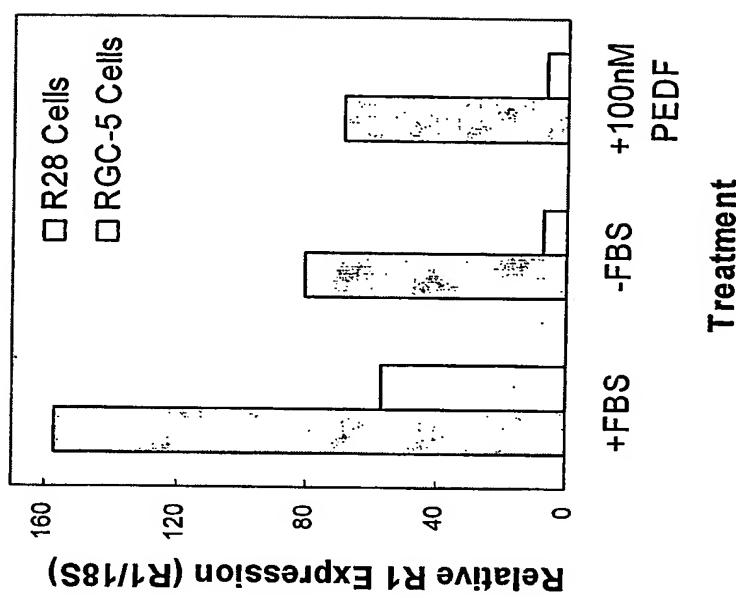


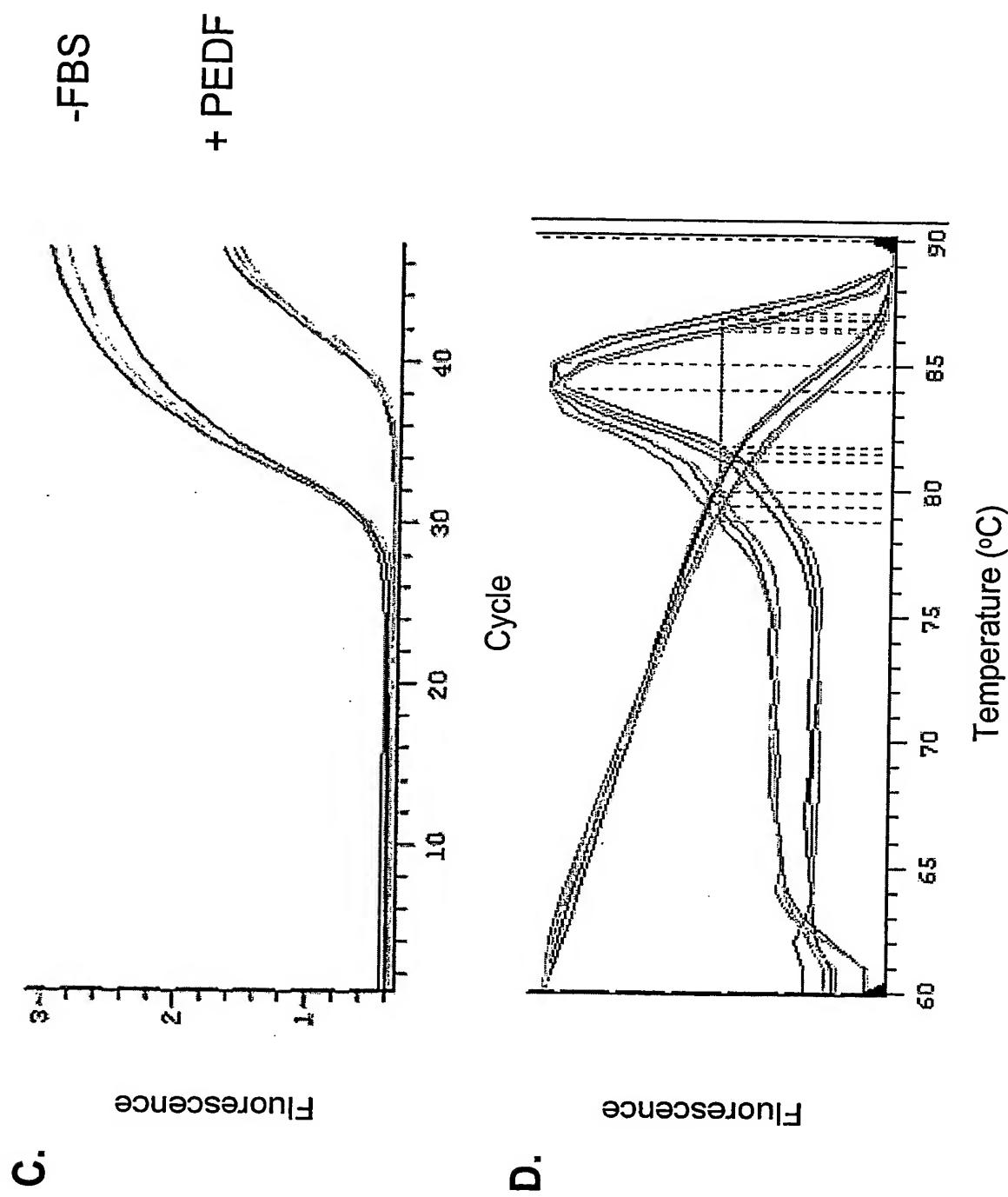
Figure 17.

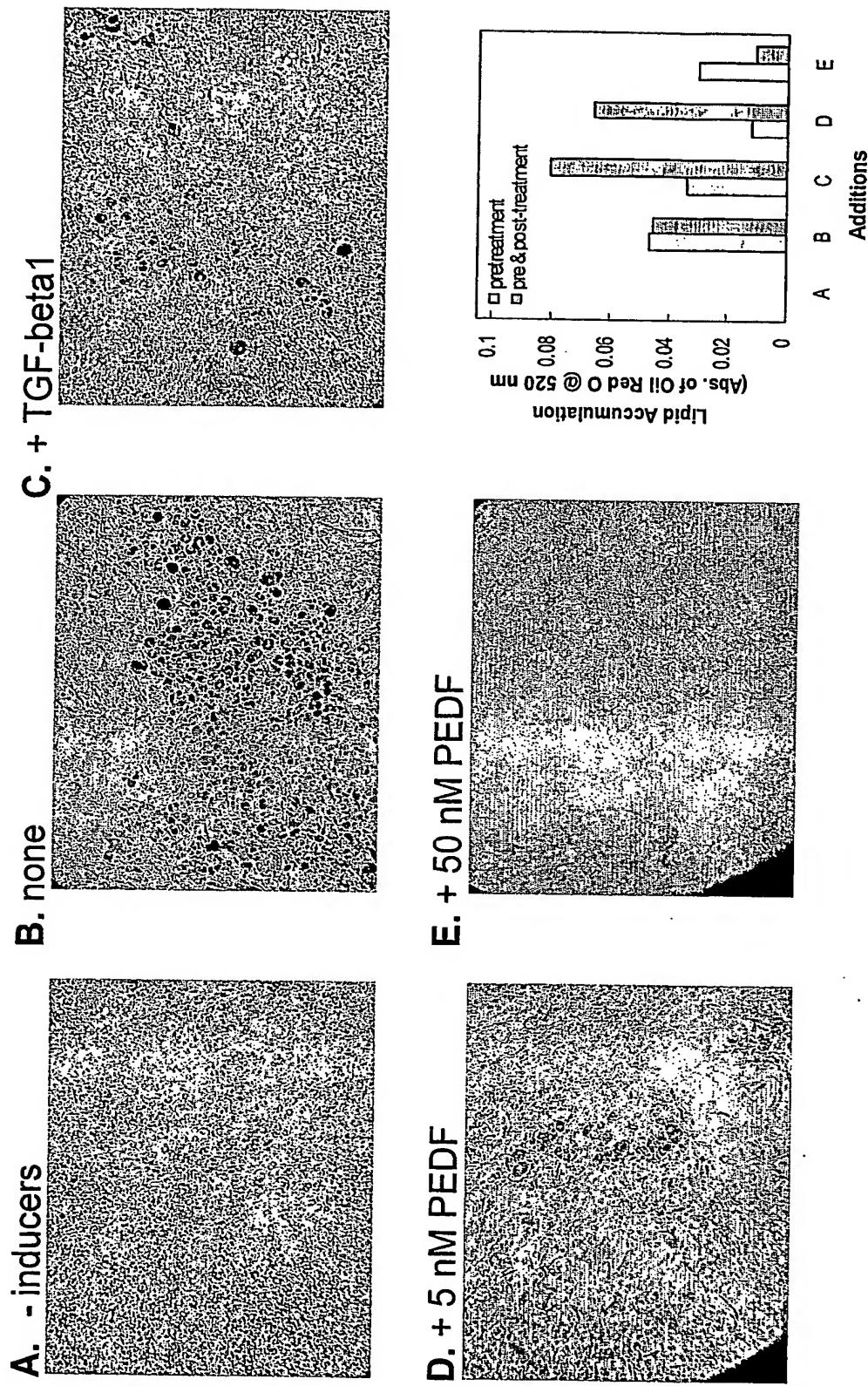
Figure 18.

Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

Figure 20. (2 of 4)

Figure 20. (3 of 4)

Figure 20. (4 of 4)

gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GTGAAACCTTCACCAGCCACTCACTATGCTACTCCTGGTGGGAGGGAT 1734 ----- GTGGGCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG 1871
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GGGGAGTCGCCCTCCCCGGAGCCCACAGAGCCCTCCCCGTACGTC-- 1782 ----- GTTTCCACACCCCTCCCCGGCCGCTGAGGCCCGCGCACCTGTGCCCT 1921
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	ACCTGTGCCCTACTCCTGCCACCA--CCTTTTCAGTGCAGGGTCAGTCT 1830 ----- AATCTCCCTCCCTGTGCTGCCGAGCACCTCCCCGCCCTTACTCC 1971
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	TAAGAACTCACATCTGCTGCTGC-TCCCTGGTGTCAAAGTTCCCTTGCA 1879 ----- TGAGAACTTTGCAGCTGCCCTCCCTCCCCGTTTTCATGGCCTGCTGAA 2021
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	GA--GTGTGTGAAGAATTATTTATTTTGCCAAAGCAGATCTAATAAAAG 1927 ----- ATATGTGTGTGAAGAATTATTTATTTGCCAAAGCACATGTAATAATG 2071
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	CCACAGCTCAGCTTCTGCCCTCCTCACTTCTGCATGCT----- 1965 ----- CTGCAGCCCCAAAAAAAAAAAAAAA 2121
gi 26327464 dbj AK031609.1 gi 34861241 ref XM_341960.1 gi 16878146 gb BC017280.1 BC01	- - A 2122